

Antman's impressive work is like no other—both a comprehensive treatise on nonlinear elasticity and a quintessential example of applied nonlinear analysis. Shortly after the appearance of the first edition, two authoritative and enthusiastic reviewers predicted it would become a standard reference in this field [3, 4]. Ten years later those predictions are now realized. A guiding theme throughout is the demand for consistent care in both the formulation and the analysis of specific classes of problems. The rigorous existence of solutions and the determination of thresholds of instability and bifurcation, classified according to nonlinear material response, are established for numerous novel problems—in most cases based upon the author's own research. The book is especially unique in its coverage of nonlinearly elastic strings, rods, and shells (of Cosserat type).

The second edition retains all the flavor of the first—and more. The text has been revised and updated. Several new sections have been added, featuring new problems for strings, planar rods, spatial rods, axisymmetric shells, and 3-d solids, expanded coverage of transverse symmetry of spatial rods, expanded coverage of general theories of rods and general theories of shells, and a new chapter on general results in 3-d nonlinear elasticity.

This book is a “must” for researchers and graduate students interested in nonlinear continuum mechanics and applied analysis. The work is scholarly and well written. The depth and breadth of coverage is staggering, and it is not for the “faint of heart.” Antman expresses this well in the preface: “This book is directed toward scientists, engineers, and mathematicians who wish to see careful treatments of uncompromised problems.”

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Knowledge Discovery in Proteomics. By Igor Jurisica and Dennis Wigle. Chapman and Hall/CRC, Boca Raton, FL, 2006. \$89.95. xxiii+318 pp., hardcover. ISBN 1-58488-439-8.

In broad terms, researchers in the life sciences are attempting to organize and understand all the processes of living organisms from the cellular to the whole organism level. Such an aim requires the accumulation of piles of data as well as novel methods for organizing and managing all that data to enable the extraction of useful information. Advancements in high-throughput (HTP) experimental techniques such as mass spectroscopy and the completion of major collaborative works like the human genome project have provided an abundant supply of data. However, the development of scalable methods for unifying the data and sifting through it to make new discoveries has been a slower process and has become a main challenge being faced.

It is not just the amount of new data available daily, but also the diversity of that data that is difficult to deal with. Biological systems are subject to various environmental conditions, any number of which can drastically alter the outcome of an experiment when perturbed. Knowing that certain proteins interact, for example, is not sufficient for our understanding if we do not also know important experimental details such as stimuli, location, and time. The issue is further complicated by difficulties with automated access and querying of diverse public databases, redundancies such as multiple names for a single protein, and missing and noisy data. When one thinks of the large number of proteins within a single cell, let alone a multicellular organism, the scale of this problem quickly becomes

overwhelming and can give one the sense of drinking from a fire hydrant.

This is where knowledge discovery plays an important role and motivates the timely publication of the book by Jurisica and Wigle. Knowledge discovery, as the authors define it, is the process of finding useful patterns in data with an emphasis on the end product of the process, which is knowledge. Naturally, this iterative process involves the management of available knowledge in a way that optimizes sharing and collaboration. However, when attempting to merge information it is difficult to determine what information is useful and what should be included. It is also difficult to plan ahead because it is impossible to predict what new methods and discoveries will be developed and lead to new data representation requirements years from now. In Chapters 1 and 2, the authors provide an overview of the knowledge discovery process with several specific examples that emphasize the usefulness of approaches that have been employed while pointing out limitations that need to be addressed. By doing so, they clearly express the need for defining standards for experimental data representation that are both comprehensive and flexible, and they motivate the discussion that follows in subsequent chapters.

The authors discuss several influential experimental and theoretical techniques employed in bioinformatics, proteomics, and systems biology today. Chapter 3 provides an introduction to mass spectrometry (MS) and an overview of the state-of-the-art MS-based experimental procedures. Some of the data processing tools and search algorithms used to manage and extract information from global proteomic studies are also described in Chapter 3. Chapters 4 and 5 go into much more depth than the other chapters and make up the majority of the content of the book. Chapter 4 is an in-depth explanation of the graph theory analysis of protein-protein interactions (PPIs). It expounds the terminology, types of network models, topological features, motifs, algorithms, and public data sets used to infer and study PPIs. Chapter 5 is a discussion of HTP protein crystallization approaches and the automated tools used to analyze and extract information from the experimental

results. Issues with diverse chemical conditions and bottlenecks in the crystallization and analysis process are also elucidated. Chapter 6 is a discussion of the approaches and tools used to integrate diverse forms of data from public databases as well as the significant issues faced and the benefits gained in that process. The book is concluded in Chapter 7 with an overview of systems biology and a description of how knowledge discovery is involved in advancing various areas of research in this field.

The authors recognize the importance of understanding how experimental and theoretical techniques interact in the knowledge discovery process; and therefore they try to strike a balance between these areas in the book. Researchers involved in the knowledge discovery process come from a variety of different backgrounds including biology, physics, mathematics, computer science, and engineering. Therefore, in order to coordinate everyone's efforts, it is necessary that researchers from all these areas understand how their results and tools will be used by others, and that they consequently optimize for sharing and collaboration. Throughout the text, impressive examples from the literature and the authors' personal research experiences highlight this key concept and point out where limitations and major challenges still exist.

The book was written by eight contributing authors with varying degrees of experience, from Ph.D. candidates to faculty members. As a result, there is a degree of disconnect between chapters in terms of writing styles as well as in the extent to which each topic is addressed. That criticism aside, this is a timely publication and, for the most part, a successful effort to depict many hot areas of research. I would highly recommend the book to new researchers, as it describes the limitations of tools and techniques being used today and draws attention to many open problems. I would also recommend the book to more experienced researchers who have a primarily theoretical or experimental bent, as attaining the goal of unifying existing knowledge will require a concerted effort from everyone involved.

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